

# SEQUENCE LISTING

<110> Dale, James B.

<120> GROUP A STREPTOCOCCAL VACCINES

<130> 481112.410

<140> US 09/151,409

<141> 1998-09-10

<150> US 60/058,635

<151> 1997-09-12

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of Synthesis -- Primer, hybridizes to streptococcal type 24 M protein DNA

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36

<210> 2

<211> 30

<212> DNA

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<223> Description of Artificial Sequence: Product of Synthesis -- Primer, hybridizes to streptococcal type 24 M protein DNA

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<213> Artificial Sequence

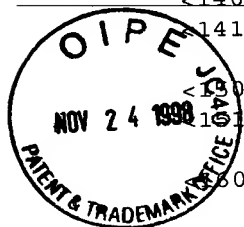
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<223> Description of Artificial Sequence: Product of Synthesis -- Primer, hybridizes to streptococcal type 5 M protein DNA

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*Sub B1*

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Synthesis -- Primer, hybridizes to streptococcal  
type 6 M protein DNA

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Synthesis -- Primer, hybridizes to streptococcal  
type 6 M protein DNA

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<210> 7  
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<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 19 M protein DNA

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<210> 8  
<211> 30  
<212> DNA  
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<223> Description of Artificial Sequence: Product of  
Synthesis -- Primer, hybridizes to streptococcal  
type 19 M protein DNA

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<400> 8  
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30

<210> 9  
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<223> Description of Artificial Sequence: Product of  
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<210> 10  
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<212> DNA  
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Synthesis -- Primer, hybridizes to streptococcal  
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<212> DNA  
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Synthesis -- Primer, hybridizes to streptococcal  
type 3 M protein DNA

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type 24 M protein DNA

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Synthesis -- Primer, hybridizes to streptococcal  
type 24 M protein DNA

<400> 14  
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DNAs

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<222> (1)..(1149)

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caa gaa cgt gct gac aag ttt gag ata gaa aac aat acg tta aaa ctt				96
Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu				
	20	25	30	
aag aat agt gac tta agt ttt aat aat aaa gcg tta aaa gat cat aat				144
Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn				
	35	40	45	
gat gag tta act gaa gag ttg agt aat gct aaa gag aaa cta cgt gga				192
Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly				
	50	55	60	
tcc gcc gtg act agg ggt aca ata aat gac ccg caa aga gca aaa gaa				240
Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu				
	65	70	75	80
gct ctt gac aag tat gag cta gaa aac cat gac tta aaa act aag aat				288
Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn				
	85	90	95	
gaa ggg tta aaa act gag aat gaa ggg tta aaa act gag aat gaa ggg				336
Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly				
	100	105	110	
tta aaa act gag aat gaa ggg tta aaa act gag gtc gac aga gtg ttt				384
Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe				
	115	120	125	
cct agg ggg acg gta gaa aac ccg gac aaa gca cga gaa ctt ctt aac				432
Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn				
	130	135	140	
aag tat gac gta gag aac tct atg tta caa gct aat aat gac aag tta				480
Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu				
	145	150	155	160
cca tgg aga gtg cgt tat act agg cat acg cca gaa gat aag cta aaa				528
Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys				
	165	170	175	
aaa att att gac gat ctt gac gca aaa gaa cat gaa tta caa caa cag				576
Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln				
	180	185	190	
aat gag aag tta tct ctg cag aac ggt gat ggt aat cct agg gaa gtt				624
Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val				
	195	200	205	
ata gaa gat ctt gca gca aac aat ccc gca ata caa aat ata cgt tta				672
Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu				
	210	215	220	
cgt cac gaa aac aag gac tta aaa gcg aga tta gag aat gca atg gaa				720
Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu				
	225	230	235	240

gtt gca gga aga gat ttt aag aga gct ggt acc ttg tta gat cag gtt	768
Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val	
245 250 255	
aca caa tta tat act aaa cat aat agt aat tac caa caa tat aat gca	816
Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala	
260 265 270	
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eaa get ggc aga ctt gac ctg aga caa aag gct gaa tat cta aaa ggc	864
Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly	
275 280 285	
ctt aat gat tgg gct gag agg ctg tta caa gag tta aat atc gat gtc	912
Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val	
290 295 300	
gcg act agg tct cag aca gat act ctg gaa aaa gta caa gaa cgt gct	960
Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala	
305 310 315 320	
gac aag ttt gag ata gaa aac aat acg tta aaa ctt aag aat agt gac	1008
Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp	
325 330 335	
tta agt ttt aat aat aaa gcg tta aaa gat cat aat gat gag tta act	1056
Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr	
340 345 350	
gaa gag ttg agt aat gct aaa gag aaa cta cgt aaa aat gat aaa tca	1104
Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser	
355 360 365	
cta tct gaa aaa gct agt aaa att caa gaa tta gag gca cgt aag	1149
Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys	
370 375 380	
taaaagctt	1158

<210> 16  
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 <212> PRT  
 <213> Artificial Sequence

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 Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu  
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 Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn  
 35 40 45  
 Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly  
 50 55 60  
 Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu

65		70		75		80									
Ala	Leu	Asp	Lys	Tyr	Glu	Leu	Glu	Asn	His	Asp	Leu	Lys	Thr	Lys	Asn
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Glu	Gly	Leu	Lys	Thr	Glu	Asn	Glu	Gly	Leu	Lys	Thr	Glu	Asn	Glu	Gly
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Leu	Lys	Thr	Glu	Asn	Glu	Gly	Leu	Lys	Thr	Glu	Val	Asp	Arg	Val	Phe
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Pro	Arg	Gly	Thr	Val	Glu	Asn	Pro	Asp	Lys	Ala	Arg	Glu	Leu	Leu	Asn
	130					135					140				
Lys	Tyr	Asp	Val	Glu	Asn	Ser	Met	Leu	Gln	Ala	Asn	Asn	Asp	Lys	Leu
145					150					155					160
Pro	Trp	Arg	Val	Arg	Tyr	Thr	Arg	His	Thr	Pro	Glu	Asp	Lys	Leu	Lys
			165						170					175	
Lys	Ile	Ile	Asp	Asp	Leu	Asp	Ala	Lys	Glu	His	Glu	Leu	Gln	Gln	Gln
			180					185					190		
Asn	Glu	Lys	Leu	Ser	Leu	Gln	Asn	Gly	Asp	Gly	Asn	Pro	Arg	Glu	Val
	195						200					205			
Ile	Glu	Asp	Leu	Ala	Ala	Asn	Asn	Pro	Ala	Ile	Gln	Asn	Ile	Arg	Leu
	210					215					220				
Arg	His	Glu	Asn	Lys	Asp	Leu	Lys	Ala	Arg	Leu	Glu	Asn	Ala	Met	Glu
225					230					235					240
Val	Ala	Gly	Arg	Asp	Phe	Lys	Arg	Ala	Gly	Thr	Leu	Leu	Asp	Gln	Val
			245						250					255	
Thr	Gln	Leu	Tyr	Thr	Lys	His	Asn	Ser	Asn	Tyr	Gln	Gln	Tyr	Asn	Ala
		260						265					270		
Gln	Ala	Gly	Arg	Leu	Asp	Leu	Arg	Gln	Lys	Ala	Glu	Tyr	Leu	Lys	Gly
	275						280					285			
Leu	Asn	Asp	Trp	Ala	Glu	Arg	Leu	Leu	Gln	Glu	Leu	Asn	Ile	Asp	Val
	290					295						300			
Ala	Thr	Arg	Ser	Gln	Thr	Asp	Thr	Leu	Glu	Lys	Val	Gln	Glu	Arg	Ala
305					310					315					320
Asp	Lys	Phe	Glu	Ile	Glu	Asn	Asn	Thr	Leu	Lys	Leu	Lys	Asn	Ser	Asp
			325					330					335		
Leu	Ser	Phe	Asn	Asn	Lys	Ala	Leu	Lys	Asp	His	Asn	Asp	Glu	Leu	Thr
		340						345					350		
Glu	Glu	Leu	Ser	Asn	Ala	Lys	Glu	Lys	Leu	Arg	Lys	Asn	Asp	Lys	Ser
	355						360					365			
Leu	Ser	Glu	Lys	Ala	Ser	Lys	Ile	Gln	Glu	Leu	Glu	Ala	Arg	Lys	
	370					375					380				